

THE RACE TEYE IDENTIFICATION AND GENETIC ANALYSIS OF SUNFLOWER BROOMRAPE IN CHINA

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Abstract

Currently, sunflower broomrape (*Orobanche cumana* Wallr.) is a parasitic seed plant and caused dramatic yield loss annually. It has become one of the most important constraints in sunflower production in China. The most effective way to control this disease is to apply resistant varieties. So, it is rather urgent to make clear the race type composition and distribution of sunflower broomrape in China, so as to facilitate the breeders to arrange the resistant varieties against different race type reasonable.

To identify the race types of *Orobanche cumana* in China, 29 samples (broomrape seeds) collected from different locations in the main sunflower production region in China. With the standard differential lines provided by Dr. Skoric, the identification tests were conducted using plastic cup under greenhouse condition. Our results showed that there are five race types of *Orobanche cumana* in China: Race A, D, E, F and G. Among them, the race G is the highest level of physiological race and all from Inner Mongolia region (Linhe, Wulateqianqi and Xixiaozhao). Race F is only found at Siwangziqi of Wulanchabu region. Race E mainly distributes in Xinjiang and Inner Mongolia. Race D is the most dominant race type, which is mainly distributed at Xinjiang, Inner Mongolia and Jinlin. Race A is mainly distributed at Shanxi, Hebei and Shaanxi and the Tuzuoqi of Inner Mongolia, where the local cultivars planted.

The genetic diversity study was performed with 96 samples from different sunflower growing areas together with 12 ISSR primers, which were screened out from 100 primers based on their high polymorphism and good reproducibility. A total of 147 bands were detected, which 90 were polymorphic bands. The percentage of polymorphic bands (PPB) was 61.22%. The genetic diversity analysis showed that the diversity of *Orobanche cumana* from Inner Mongolia and Xinjiang was relatively higher. The Shannon diversity index was 0.5560 and 0.5067 respectively. The cluster analysis showed that the *Orobanche cumana* from 6 different provinces can be divided into two subgroups, of which Shanxi, Shaanxi and Hebei provinces were clustered into one subgroup. Jilin, Inner Mongolia and Xinjiang were clustered into another subgroup. The genetic distance between Shanxi and Hebei was the closest, while distance between Hebei and Xinjiang was the longest.

Keywords: sunflower, *Orobanche cumana*, race type identification, genetic variation